SEQUENCE LISTING

<110> Salceda, Susana
Sun, Yongming
Recipon, Herve
Cafferkey, Robert

<120> A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING, IMAGING AND TREATING VARIOUS CANCERS

<130> DEX-0172

<140> 09/763,978
<141> 2001-02-28

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<150> 60/098,880
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cacttcgcaa ctcaggggcg gctgcatttt agtaatgggt caaatgattc acttttatg 360

atgcttccaa aggtgccttg gcttctcttc ccaactgaca aatgccaaag ttgagaaaaa 420

tgatcataat tttagcataa acagagcagt cggcgacacc gattttataa ataaactgag 480

caccttcttt ttaaacaaac aaatgcgggt ttatttctca gatgatgttc atccgtgaat 540

ggtccaggga aggacctttc accttgacta tatggc 576

<210> 11
<211> 890
<212> DNA
<213> Homo sapien

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tgaagacaat tttggttacc tcaatgaggg agtggaggag gatacagtgc tactaccaac 180

tagtggataa aggccaggga tgctgctcaa cctcctacca tgtacaggga cgtctcccca 240

ttacaactac ccaatccgaa gtgtcaactg tgtcaggact aagaaaccct ggttttgagt 300

agaaaagggc ctggaaagag gggagccaac aaatctgtct gcttcctcac attagtcatt 360

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gggcaccagg ataacatctc tcagtgaaca gagttgacaa ggcctatggg aaatgcctga 480

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tctccagacc cttcctggcc acaattcaaa ttaaggcaac aaacatatac cttccatgaa 660

gcacacacag acttttgaaa gcaaggacaa tgactgcttg aattgaggcc ttgaggaatg 720

aagctttgaa ggaaaagaat actttgtttc cagccccctt cccacactct tcatgtgtta 780

accactgcct tcctggacct tggagccacg gtgactgtat tacatgttgt tatagaaaac 840

tgattttaga gttctgatcg ttcaagagaa tgattaaata tacatttcct 890

<210> 12
<211> 406
<212> DNA
<213> Homo sapien

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<222> (30)..(30)
<223> n= a, c, g, or t

<220>
<221> misc_feature
<222> (248)..(248)
<223> n= a, c, g, or t

<220>
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<223> n= a, c, g, or t

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tccaatacca gctttgagct gaactctgag aatgtgacca tgaaggttgt gtctgtgctc 180

tacaatgtta cgatcaacaa cacatactcc tgtatgattg aaaatgacat tgccaaagca 240

acaggggnta tcaaagtgac agaatcggag atcaaaaggc ggagtcacct acagctgcta 300

aactcaaagg cttctctgtg tgtctcttct ttctttgcca tcagctgggc acttctgcct 360

ctcagccctt acctgatgct aanataatgt gccttggcca caaaaa 406

<210> 13
<211> 462
<212> DNA
<213> Homo sapien

<400> 13
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ggagcaattg cactcatcat tggctttggt atttcaggga gacactccat cacagtcact 180

actgtcgcct cagctgggaa cattggggag gatggaatcc tgagctgcac ttttgaacct 240

gacatcaaac tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 300

catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt cagaggccgg 360

acagcagtgt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct gaaaaacgtg 420

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<211> 272
<212> DNA
<213> Homo sapien

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ggaggatcac agagccagca tggatcctga cagtgatcaa cctctgaaca gcctcgtcaa 240

ggtgattctg gataaatact acttcctctg cg 272

<210> 15
<211> 492
<212> PRT
<213> Homo sapien

<400> 15

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Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
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Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
35 40 45

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80

Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
100 105 110

Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
115 120 125

Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
130 135 140

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Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145                 150                 155                 160

Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
                165                 170                 175

Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
            180                 185                 190

Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
        195                 200                 205

Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
    210                 215                 220

Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225                 230                 235                 240

Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
                245                 250                 255

Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
            260                 265                 270

Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
        275                 280                 285

Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
    290                 295                 300

Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305                 310                 315                 320

Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
                325                 330                 335

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
            340                 345                 350

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
        355                 360                 365

Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
    370                 375                 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
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385 390 395 400

Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
405 410 415

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
435 440 445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
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Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
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<210> 16
<211> 890
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnncat 240

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tctccagacc ctgcctggcc acaattcaaa ttaaggcaac aaacatatac cttccatgaa 660

gcacacacag acttttgaaa gcaaggacaa tgactgcttg aattgaggcc ttgaggaatg 720

aagctttgaa ggaaaagaat actttgtttc agccccctt cccacactct tcatgtgtta 780

accactgcct tcctggacct tggagccacg gtgactgtat tacatgttgt tatagaaaac 840

tgattttaga gttctgatcg ttcaagagaa tgattaaata tacatttcct 890